Niels Grarup

List of Publications by Citations

259 papers	22,968 citations	70 h-index	149 g-index
285 ext. papers	28,676 ext. citations	12 avg, IF	5.41 L-index

#	Paper	IF	Citations
259	Richness of human gut microbiome correlates with metabolic markers. *Nature*, **2013**, 500, 541-6	50.4	2584
258	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
257	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
256	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
255	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
254	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. *Nature Genetics*, **2018**, 50, 1505-1513	36.3	675
253	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
252	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
251	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
250	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
249	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. *Nature Genetics*, **2015**, 47, 1449-1456	36.3	329
248	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. *PLoS Genetics*, **2012**, 8, e1002607	6	326
247	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
246	Greenlandic Inuit show genetic signatures of diet and climate adaptation. *Science*, **2015**, 349, 1343-7	33.3	298
245	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
244	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
243	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. *Nature Genetics*, **2010**, 42, 969-72	36.3	264

242	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. *Nature*, **2014**, 512, 190-3	50.4	258
241	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. *Nature Genetics*, **2014**, 46, 294-8	36.3	241
240	Impact of type 2 diabetes susceptibility variants on quantitative glycemic traits reveals mechanistic heterogeneity. *Diabetes*, **2014**, 63, 2158-71	0.9	235
239	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 97-105	18.1	225
238	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
237	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
236	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
235	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. *Nature Genetics*, **2010**, 42, 864-8	36.3	214
234	Studies of association of variants near the HHEX, CDKN2A/B, and IGF2BP2 genes with type 2 diabetes and impaired insulin release in 10,705 Danish subjects: validation and extension of genome-wide association studies. *Diabetes*, **2007**, 56, 3105-11	0.9	207
233	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
232	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
231	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
230	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
229	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
228	Common type 2 diabetes risk gene variants associate with gestational diabetes. *Journal of Clinical Endocrinology and Metabolism*, **2009**, 94, 145-50	5.6	169
227	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. *Nature Genetics*, **2010**, 42, 692-7	36.3	155
226	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
225	Gene physical activity interactions in obesity: combined analysis of 111,421 individuals of European ancestry. *PLoS Genetics*, **2013**, 9, e1003607	6	145

224	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
223	Genetic susceptibility to type 2 diabetes and obesity: from genome-wide association studies to rare variants and beyond. *Diabetologia*, **2014**, 57, 1528-41	10.3	135
222	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. *Nature*, **2019**, 570, 71-76	50.4	129
221	Estimation of allele frequency and association mapping using next-generation sequencing data. *BMC Bioinformatics*, **2011**, 12, 231	3.6	126
220	FGF21 Is a Sugar-Induced Hormone Associated with Sweet Intake and Preference in Humans. *Cell Metabolism*, **2017**, 25, 1045-1053.e6	24.6	123
219	Apolipoprotein(a) genetic sequence variants associated with systemic atherosclerosis and coronary atherosclerotic burden but not with venous thromboembolism. *Journal of the American College of Cardiology*, **2012**, 60, 722-9	15.1	118
218	Association testing of novel type 2 diabetes risk alleles in the JAZF1, CDC123/CAMK1D, TSPAN8, THADA, ADAMTS9, and NOTCH2 loci with insulin release, insulin sensitivity, and obesity in a population-based sample of 4,516 glucose-tolerant middle-aged Danes. *Diabetes*, **2008**, 57, 2534-40	0.9	116
217	Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. *Nature Genetics*, **2019**, 51, 1137-1148	36.3	111
216	G-allele of intronic rs10830963 in MTNR1B confers increased risk of impaired fasting glycemia and type 2 diabetes through an impaired glucose-stimulated insulin release: studies involving 19,605 Europeans. *Diabetes*, **2009**, 58, 1450-6	0.9	111
215	Whole-exome sequencing of 2,000 Danish individuals and the role of rare coding variants in type 2 diabetes. *American Journal of Human Genetics*, **2013**, 93, 1072-86	11	109
214	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
213	Natural selection affects multiple aspects of genetic variation at putatively neutral sites across the human genome. *PLoS Genetics*, **2011**, 7, e1002326	6	107
212	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
211	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
210	Exome sequencing-driven discovery of coding polymorphisms associated with common metabolic phenotypes. *Diabetologia*, **2013**, 56, 298-310	10.3	102
209	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. *Nature Communications*, **2016**, 7, 10531	17.4	99
208	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. *Nature Genetics*, **2018**, 50, 172-174	36.3	97
207	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96

206	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
205	Variant ASGR1 Associated with a Reduced Risk of Coronary Artery Disease. *New England Journal of Medicine*, **2016**, 374, 2131-41	59.2	94
204	Studies of the relationship between the ENPP1 K121Q polymorphism and type 2 diabetes, insulin resistance and obesity in 7,333 Danish white subjects. *Diabetologia*, **2006**, 49, 2097-104	10.3	91
203	Genome-wide population-based association study of extremely overweight young adults--the GOYA study. *PLoS ONE*, **2011**, 6, e24303	3.7	90
202	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
201	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
200	Genetic evidence of a causal effect of insulin resistance on branched-chain amino acid levels. *Diabetologia*, **2017**, 60, 873-878	10.3	79
199	Whole-Exome Sequencing of 2,000 Danish Individuals and the Role of Rare Coding Variants in Type 2 Diabetes. *American Journal of Human Genetics*, **2014**, 94, 479	11	78
198	EHMTI-0380. The association of migraine susceptibility loci with severe migraine characteristics in a clinic-based migraine sample. *Journal of Headache and Pain*, **2014**, 15,	8.8	78
197	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
196	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. *PLoS Genetics*, **2015**, 11, e1004876	6	76
195	Variants at DGKB/TMEM195, ADRA2A, GLIS3 and C2CD4B loci are associated with reduced glucose-stimulated beta cell function in middle-aged Danish people. *Diabetologia*, **2010**, 53, 1647-55	10.3	76
194	Habitual sleep duration is associated with BMI and macronutrient intake and may be modified by CLOCK genetic variants. *American Journal of Clinical Nutrition*, **2015**, 101, 135-43	7	75
193	Genome-wide analyses identify a role for SLC17A4 and AADAT in thyroid hormone regulation. *Nature Communications*, **2018**, 9, 4455	17.4	75
192	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. *PLoS Genetics*, **2013**, 9, e1003530	6	72
191	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. *Diabetes*, **2018**, 67, 1414-1427	0.9	71
190	Genomewide meta-analysis identifies loci associated with IGF-I and IGFBP-3 levels with impact on age-related traits. *Aging Cell*, **2016**, 15, 811-24	9.9	71
189	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. *Diabetes*, **2017**, 66, 2296-2309	0.9	69

188	Variants near MC4R are associated with obesity and influence obesity-related quantitative traits in a population of middle-aged people: studies of 14,940 Danes. *Diabetes*, **2009**, 58, 757-64	0.9	69
187	Cardiolipin Synthesis in Brown and Beige Fat Mitochondria Is Essential for Systemic Energy Homeostasis. *Cell Metabolism*, **2018**, 28, 159-174.e11	24.6	67
186	Uncovering the genetic history of the present-day Greenlandic population. *American Journal of Human Genetics*, **2015**, 96, 54-69	11	61
185	Underlying genetic models of inheritance in established type 2 diabetes associations. *American Journal of Epidemiology*, **2009**, 170, 537-45	3.8	60
184	Replication and meta-analysis of common variants identifies a genome-wide significant locus in migraine. *European Journal of Neurology*, **2013**, 20, 765-72	6	59
183	First Genome-Wide Association Study of Latent Autoimmune Diabetes in Adults Reveals Novel Insights Linking Immune and Metabolic Diabetes. *Diabetes Care*, **2018**, 41, 2396-2403	14.6	57
182	Type 2 diabetes risk alleles near ADCY5, CDKAL1 and HHEX-IDE are associated with reduced birthweight. *Diabetologia*, **2010**, 53, 1908-16	10.3	56
181	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. *American Journal of Human Genetics*, **2019**, 104, 112-138	11	54
180	Combined analyses of 20 common obesity susceptibility variants. *Diabetes*, **2010**, 59, 1667-73	0.9	51
179	Combined analysis of 19 common validated type 2 diabetes susceptibility gene variants shows moderate discriminative value and no evidence of gene-gene interaction. *Diabetologia*, **2009**, 52, 1308-14	10.3	51
178	Studies of the common DIO2 Thr92Ala polymorphism and metabolic phenotypes in 7342 Danish white subjects. *Journal of Clinical Endocrinology and Metabolism*, **2007**, 92, 363-6	5.6	51
177	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. *Molecular Biology and Evolution*, **2017**, 34, 1307-1318	8.3	50
176	A genetic risk score of 45 coronary artery disease risk variants associates with increased risk of myocardial infarction in 6041 Danish individuals. *Atherosclerosis*, **2015**, 240, 305-10	3.1	50
175	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. *Nature Communications*, **2018**, 9, 321	17.4	50
174	Dysregulation of a long noncoding RNA reduces leptin leading to a leptin-responsive form of obesity. *Nature Medicine*, **2019**, 25, 507-516	50.5	49
173	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. *Cell Reports*, **2018**, 23, 327-336	10.6	48
172	Gene-environment interactions in the pathogenesis of type 2 diabetes and metabolism. *Current Opinion in Clinical Nutrition and Metabolic Care*, **2007**, 10, 420-6	3.8	48
171	Causal relationship between obesity and serum testosterone status in men: A bi-directional mendelian randomization analysis. *PLoS ONE*, **2017**, 12, e0176277	3.7	47

170	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. *Diabetes*, **2016**, 65, 3200-11	0.9	47
169	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
168	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
167	Type 2 diabetes risk alleles near BCAR1 and in ANK1 associate with decreased □cell function whereas risk alleles near ANKRD55 and GRB14 associate with decreased insulin sensitivity in the Danish Inter99 cohort. *Journal of Clinical Endocrinology and Metabolism*, **2013**, 98, E801-6	5.6	46
166	Obesity, unfavourable lifestyle and genetic risk of type 2 diabetes: a case-cohort study. *Diabetologia*, **2020**, 63, 1324-1332	10.3	46
165	Rare genetic variants previously associated with congenital forms of long QT syndrome have little or no effect on the QT interval. *European Heart Journal*, **2015**, 36, 2523-9	9.5	45
164	Identification of KCNJ15 as a susceptibility gene in Asian patients with type 2 diabetes mellitus. *American Journal of Human Genetics*, **2010**, 86, 54-64	11	45
163	Genetic investigations of sudden unexpected deaths in infancy using next-generation sequencing of 100 genes associated with cardiac diseases. *European Journal of Human Genetics*, **2016**, 24, 817-22	5.3	44
162	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
161	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
160	Variant near ADAMTS9 known to associate with type 2 diabetes is related to insulin resistance in offspring of type 2 diabetes patients--EUGENE2 study. *PLoS ONE*, **2009**, 4, e7236	3.7	43
159	Physiologic characterization of type 2 diabetes-related loci. *Current Diabetes Reports*, **2010**, 10, 485-97	5.6	41
158	Studies of the association of Arg72Pro of tumor suppressor protein p53 with type 2 diabetes in a combined analysis of 55,521 Europeans. *PLoS ONE*, **2011**, 6, e15813	3.7	41
157	A glycogene mutation map for discovery of diseases of glycosylation. *Glycobiology*, **2015**, 25, 211-24	5.8	38
156	MTNR1B G24E variant associates With BMI and fasting plasma glucose in the general population in studies of 22,142 Europeans. *Diabetes*, **2010**, 59, 1539-48	0.9	37
155	Variation in the peroxisome proliferator-activated receptor delta gene in relation to common metabolic traits in 7,495 middle-aged white people. *Diabetologia*, **2007**, 50, 1201-8	10.3	37
154	Gene-Environment Interactions of Circadian-Related Genes for Cardiometabolic Traits. *Diabetes Care*, **2015**, 38, 1456-66	14.6	36
153	Association of variants in the sterol regulatory element-binding factor 1 (SREBF1) gene with type 2 diabetes, glycemia, and insulin resistance: a study of 15,734 Danish subjects. *Diabetes*, **2008**, 57, 1136-42	0.9	36

152	Type 2 diabetes risk allele near CENTD2 is associated with decreased glucose-stimulated insulin release. *Diabetologia*, **2011**, 54, 1052-6	10.3	34
151	Meta-analysis of rare and common exome chip variants identifies S1PR4 and other loci influencing blood cell traits. *Nature Genetics*, **2016**, 48, 867-76	36.3	34
150	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
149	What is the contribution of two genetic variants regulating VEGF levels to type 2 diabetes risk and to microvascular complications?. *PLoS ONE*, **2013**, 8, e55921	3.7	32
148	The Effect of an Extreme and Prolonged Population Bottleneck on Patterns of Deleterious Variation: Insights from the Greenlandic Inuit. *Genetics*, **2017**, 205, 787-801	4	31
147	Association studies of novel obesity-related gene variants with quantitative metabolic phenotypes in a population-based sample of 6,039 Danish individuals. *Diabetologia*, **2012**, 55, 105-13	10.3	31
146	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
145	A trans-ancestral meta-analysis of genome-wide association studies reveals loci associated with childhood obesity. *Human Molecular Genetics*, **2019**, 28, 3327-3338	5.6	30
144	Common variation in LMNA increases susceptibility to type 2 diabetes and associates with elevated fasting glycemia and estimates of body fat and height in the general population: studies of 7,495 Danish whites. *Diabetes*, **2007**, 56, 694-8	0.9	30
143	Diabetic microvascular complications are not associated with two polymorphisms in the GLUT-1 and PC-1 genes regulating glucose metabolism in Caucasian type 1 diabetic patients. *Nephrology Dialysis Transplantation*, **2001**, 16, 1653-6	4.3	30
142	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
141	Estimating the causal effect of body mass index on hay fever, asthma and lung function using Mendelian randomization. *Allergy: European Journal of Allergy and Clinical Immunology*, **2018**, 73, 153-164	9.3	28
140	A variant in the G6PC2/ABCB11 locus is associated with increased fasting plasma glucose, increased basal hepatic glucose production and increased insulin release after oral and intravenous glucose loads. *Diabetologia*, **2009**, 52, 2122-9	10.3	28
139	The -250G>A promoter variant in hepatic lipase associates with elevated fasting serum high-density lipoprotein cholesterol modulated by interaction with physical activity in a study of 16,156 Danish subjects. *Journal of Clinical Endocrinology and Metabolism*, **2008**, 93, 2294-9	5.6	27
138	The diabetogenic VPS13C/C2CD4A/C2CD4B rs7172432 variant impairs glucose-stimulated insulin response in 5,722 non-diabetic Danish individuals. *Diabetologia*, **2011**, 54, 789-94	10.3	26
137	Glucose tolerance, insulin sensitivity and insulin release in European non-diabetic carriers of a polymorphism upstream of CDKN2A and CDKN2B. *Diabetologia*, **2011**, 54, 795-802	10.3	26
136	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
135	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25

134	Interactions of Lipid Genetic Risk Scores With Estimates of Metabolic Health in a Danish Population. *Circulation: Cardiovascular Genetics*, **2015**, 8, 465-72		25
133	The PNPLA3 rs738409 G-allele associates with reduced fasting serum triglyceride and serum cholesterol in Danes with impaired glucose regulation. *PLoS ONE*, **2012**, 7, e40376	3.7	25
132	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
131	Investigating the causal effect of smoking on hay fever and asthma: a Mendelian randomization meta-analysis in the CARTA consortium. *Scientific Reports*, **2017**, 7, 2224	4.9	24
130	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
129	Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. *BMJ, The*, **2019**, 366, l4292	5.9	23
128	MTHFR C677T genotype and cardiovascular risk in a general population without mandatory folic acid fortification. *European Journal of Nutrition*, **2014**, 53, 1549-59	5.2	23
127	High Prevalence of Diabetes-Predisposing Variants in MODY Genes Among Danish Women With Gestational Diabetes Mellitus. *Journal of the Endocrine Society*, **2017**, 1, 681-690	0.4	23
126	Variation and association to diabetes in 2000 full mtDNA sequences mined from an exome study in a Danish population. *European Journal of Human Genetics*, **2014**, 22, 1040-5	5.3	23
125	Lipolysis drives expression of the constitutively active receptor GPR3 to induce adipose thermogenesis. *Cell*, **2021**, 184, 3502-3518.e33	56.2	23
124	Genetic determinants of serum vitamin B12 and their relation to body mass index. *European Journal of Epidemiology*, **2017**, 32, 125-134	12.1	22
123	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
122	Carriers of the TCF7L2 rs7903146 TT genotype have elevated levels of plasma glucose, serum proinsulin and plasma gastric inhibitory polypeptide (GIP) during a meal test. *Diabetologia*, **2011**, 54, 103-10	10.3	22
121	No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. *Diabetes*, **2012**, 61, 1291-6	0.9	21
120	Genetic variability of the SUR1 promoter in relation to beta-cell function and Type II diabetes mellitus. *Diabetologia*, **2001**, 44, 1330-4	10.3	21
119	Numerous Brugada syndrome-associated genetic variants have no effect on J-point elevation, syncope susceptibility, malignant cardiac arrhythmia, and all-cause mortality. *Genetics in Medicine*, **2017**, 19, 521-528	8.1	20
118	The KCNMB1 Glu65Lys polymorphism associates with reduced systolic and diastolic blood pressure in the Inter99 study of 5729 Danes. *Journal of Hypertension*, **2008**, 26, 2142-6	1.9	20
117	Do gene variants influencing adult adiposity affect birth weight? A population-based study of 24 loci in 4,744 Danish individuals. *PLoS ONE*, **2010**, 5, e14190	3.7	20

116	Bioinformatics-driven identification and examination of candidate genes for non-alcoholic fatty liver disease. *PLoS ONE*, **2011**, 6, e16542	3.7	19
115	The association between candidate migraine susceptibility loci and severe migraine phenotype in a clinical sample. *Cephalalgia*, **2016**, 36, 615-23	6.1	18
114	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. *European Journal of Human Genetics*, **2019**, 27, 952-962	5.3	18
113	The Early Growth Genetics (EGG) and EArly Genetics and Lifecourse Epidemiology (EAGLE) consortia: design, results and future prospects. *European Journal of Epidemiology*, **2019**, 34, 279-300	12.1	18
112	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18
111	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017** , 26, 2346-2363	5.6	17
110	Discovery of coding genetic variants influencing diabetes-related serum biomarkers and their impact on risk of type 2 diabetes. *Journal of Clinical Endocrinology and Metabolism*, **2015**, 100, E664-71	5.6	17
109	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. *PLoS Genetics*, **2015**, 11, e1005379	6	17
108	Genetics of Type 2 Diabetes: the Power of Isolated Populations. *Current Diabetes Reports*, **2016**, 16, 65	5.6	17
107	A novel rare CUBN variant and three additional genes identified in Europeans with and without diabetes: results from an exome-wide association study of albuminuria. *Diabetologia*, **2019**, 62, 292-305	10.3	17
106	Genetic Variations in the Human G Protein-coupled Receptor Class C, Group 6, Member A (GPRC6A) Control Cell Surface Expression and Function. *Journal of Biological Chemistry*, **2017**, 292, 1524-1534	5.4	16
105	Abdominal adiposity and cardiometabolic risk factors in children and adolescents: a Mendelian randomization analysis. *American Journal of Clinical Nutrition*, **2019**, 110, 1079-1087	7	16
104	Genetic variant SLC2A2 [corrected] Is associated with risk of cardiovascular disease assessing the individual and cumulative effect of 46 type 2 diabetes related genetic variants. *PLoS ONE*, **2012**, 7, e50418	3.7	16
103	PC-1 amino acid variant (K121Q) has no impact on progression of diabetic nephropathy in type 1 diabetic patients. *Nephrology Dialysis Transplantation*, **2002**, 17, 1408-12	4.3	16
102	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
101	Identification of Novel Genetic Determinants of Erythrocyte Membrane Fatty Acid Composition among Greenlanders. *PLoS Genetics*, **2016**, 12, e1006119	6	16
100	Urinary metabolomics reveals glycemic and coffee associated signatures of thyroid function in two population-based cohorts. *PLoS ONE*, **2017**, 12, e0173078	3.7	15
99	The type 2 diabetes risk allele of TMEM154-rs6813195 associates with decreased beta cell function in a study of 6,486 Danes. *PLoS ONE*, **2015**, 10, e0120890	3.7	15

98	Comparative Analyses of QTLs Influencing Obesity and Metabolic Phenotypes in Pigs and Humans. *PLoS ONE*, **2015**, 10, e0137356	3.7	15
97	Skeletal muscle enhancer interactions identify genes controlling whole-body metabolism. *Nature Communications*, **2020**, 11, 2695	17.4	14
96	Homozygous carriers of the G allele of rs4664447 of the glucagon gene (GCG) are characterised by decreased fasting and stimulated levels of insulin, glucagon and glucagon-like peptide (GLP)-1. *Diabetologia*, **2011**, 54, 2820-31	10.3	14
95	A genome-wide association study of thyroid stimulating hormone and free thyroxine in Danish children and adolescents. *PLoS ONE*, **2017**, 12, e0174204	3.7	14
94	Functional and genetic epidemiological characterisation of the FFAR4 (GPR120) p.R270H variant in the Danish population. *Journal of Medical Genetics*, **2016**, 53, 616-23	5.8	14
93	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. *Circulation Genomic and Precision Medicine*, **2018**, 11, e001758	5.2	14
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